21978 Protein Sequences PCT SEQUENCE LISTING

<110> INSERM

SANOFI-AVENTIS

<120> USE OF ANTAGONISTS TO THE CB1 RECEPTOR FOR THE MANUFACTURE OF A COMPOSITION USEFUL FOR THE TREATMENT OF HEPATIC DISEASES

<130> CB1

<150> EP04290633

<151> 2004-03-09

<160> 9

<170> PatentIn version 3.1

<210> 1

<211> 472

<212> PRT

<213> Human

<400> 1

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Ile Lys Gly Asp Met Ala Ser Lys Leu Gly Tyr Phe Pro Gln Lys Phe 35 40 45

Pro Leu Thr Ser Phe Arg Gly Ser Pro Phe Gln Glu Lys Met Thr Ala 50 55 60

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Gly Asp Asn Pro Gln Leu Val Pro Ala Asp Gln Val Asn Ile Thr Glu 65 70 75 80

Phe Tyr Asn Lys Ser Leu Ser Ser Phe Lys Glu Asn Glu Glu Asn Ile 85 90 95

Gln Cys Gly Glu Asn Phe Met Asp Ile Glu Cys Phe Met Val Leu Asn 100 105 110

Pro Ser Gln Gln Leu Ala Ile Ala Val Leu Ser Leu Thr Leu Gly Thr 115 120 125

Phe Thr Val Leu Glu Asn Leu Leu Val Leu Cys Val Ile Leu His Ser 130 135 140

Arg Ser Leu Arg Cys Arg Pro Ser Tyr His Phe Ile Gly Ser Leu Ala 145 150 155 160

Val Ala Asp Leu Cly Ser Val Ile Phe Val Tyr Ser Phe Ile Asp 165 170 175

Phe His Val Phe His Arg Lys Asp Ser Arg Asn Val Phe Leu Phe Lys 180 185 190

Leu Gly Gly Val Thr Ala Ser Phe Thr Ala Ser Val Gly Ser Leu Phe 195 200 205

Leu Thr Ala Ile Asp Arg Tyr Ile Ser Ile His Arg Pro Leu Ala Tyr 210 215 220

Lys Arg Ile Val Thr Arg Pro Lys Ala Val Val Ala Phe Cys Leu Met 225 230 235 240

Trp Thr Ile Ala Ile Val Ile Ala Val Leu Pro Leu Leu Gly Trp Asn 245 250 255

Cys Glu Lys Leu Gln Ser Val Cys Ser Asp Ile Phe Pro His Ile Asp 260 265 270

Glu Thr Tyr Leu Met Phe Trp Ile Gly Val Thr Ser Val Leu Leu Leu 275 280 285

Phe Ile Val Tyr Ala Tyr Met Tyr Ile Leu Trp Lys Ala His Ser His 290 295 300

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Ala Val Arg Met Ile Gln Arg Gly Thr Gln Lys Ser Ile Ile Ile His 305 310 315 320

Thr Ser Glu Asp Gly Lys Val Gln Val Thr Arg Pro Asp Gln Ala Arg 325 330 335

Met Asp Ile Arg Leu Ala Lys Thr Leu Val Leu Ile Leu Val Val Leu 340 345 350

Ile Ile Cys Trp Gly Pro Leu Leu Ala Ile Met Val Tyr Asp Val Phe 355 360 365

Gly Lys Met Asn Lys Leu Ile Lys Thr Val Phe Ala Phe Cys Ser Met 370 375 380

Leu Cys Leu Leu Asn Ser Thr Val Asn Pro Ile Ile Tyr Ala Leu Arg 385 390 395 400

Ser Lys Asp Leu Arg His Ala Phe Arg Ser Met Phe Pro Ser Cys Glu 405 410 415

Gly Thr Ala Gln Pro Leu Asp Asn Ser Met Gly Asp Ser Asp Cys Leu 420 425 430

His Lys His Ala Asn Asn Ala Ala Ser Val His Arg Ala Ala Glu Ser 435 440 445

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Thr Asp Thr Ser Ala Glu Ala Leu 465 470

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Glu Asn Ile Gln Cys Gly Glu Asn Phe Met Asp Ile Glu Cys Phe Met
35 40 45

Val Leu Asn Pro Ser Gln Gln Leu Ala Ile Ala Val Leu Ser Leu Thr 50 55 60

Leu Gly Thr Phe Thr Val Leu Glu Asn Leu Leu Val Leu Cys Val Ile 65 70 75 80

Leu His Ser Arg Ser Leu Arg Cys Arg Pro Ser Tyr His Phe Ile Gly 85 90 95

Ser Leu Ala Val Ala Asp Leu Leu Gly Ser Val Ile Phe Val Tyr Ser 100 105 110

Phe Ile Asp Phe His Val Phe His Arg Lys Asp Ser Arg Asn Val Phe 115 120 125

Leu Phe Lys Leu Gly Gly Val Thr Ala Ser Phe Thr Ala Ser Val Gly 130 135 140

Ser Leu Phe Leu Thr Ala Ile Asp Arg Tyr Ile Ser Ile His Arg Pro 145 150 155 160

Leu Ala Tyr Lys Arg Ile Val Thr Arg Pro Lys Ala Val Val Ala Phe 165 170 175

Cys Leu Met Trp Thr Ile Ala Ile Val Ile Ala Val Leu Pro Leu Leu 180 185 190

Gly Trp Asn Cys Glu Lys Leu Gln Ser Val Cys Ser Asp Ile Phe Pro 195 200 205

His Ile Asp Glu Thr Tyr Leu Met Phe Trp Ile Gly Val Thr Ser Val 210 215 220

Leu Leu Leu Phe Ile Val Tyr Ala Tyr Met Tyr Ile Leu Trp Lys Ala 225 230 235 240

His Ser His Ala Val Arg Met Ile Gln Arg Gly Thr Gln Lys Ser Ile 245 250 255

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Ile Ile His Thr Ser Glu Asp Gly Lys Val Gln Val Thr Arg Pro Asp 260 265 270

Gln Ala Arg Met Asp Ile Arg Leu Ala Lys Thr Leu Val Leu Ile Leu 275 280 285

Val Val Leu Ile Ile Cys Trp Gly Pro Leu Leu Ala Ile Met Val Tyr 290 295 300

Asp Val Phe Gly Lys Met Asn Lys Leu Ile Lys Thr Val Phe Ala Phe 305 310 315 320

Cys Ser Met Leu Cys Leu Leu Asn Ser Thr Val Asn Pro Ile Ile Tyr 325 330 335

Ala Leu Arg Ser Lys Asp Leu Arg His Ala Phe Arg Ser Met Phe Pro 340 345 350

Ser Cys Glu Gly Thr Ala Gln Pro Leu Asp Asn Ser Met Gly Asp Ser 355 360 365

Asp Cys Leu His Lys His Ala Asn Asn Ala Ala Ser Val His Arg Ala 370 375 380

Ala Glu Ser Cys Ile Lys Ser Thr Val Lys Ile Ala Lys Val Thr Met 385 390 395 400

Ser Val Ser Thr Asp Thr Ser Ala Glu Ala Leu 405 410

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Gln Tyr Glu Asp 20

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<212> PRT

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Glu Asp Gly Lys 20

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Cys Ile Lys Ser

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His Lys His Ala Asn Asn Thr Ala Ser Met His Arg Ala Ala Glu Ser 10 15

Cys Ile Lys Ser